

=> d his full

(FILE 'HOME' ENTERED AT 09:16:58 ON 30 DEC 2005)

FILE 'BIOSIS, MEDLINE, CAPLUS' ENTERED AT 09:17:45 ON 30 DEC 2005
L1 1 SEA ALUSTXA OR ALUSTXY
D L1 AB BIB
L2 331 SEA DETERMIN? AND GENDER AND LOCUS
L3 0 SEA L2 AND (SEX 5A TYPING)

FILE HOME

FILE BIOSIS
FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 28 December 2005 (20051228/ED)

FILE MEDLINE

FILE LAST UPDATED: 29 DEC 2005 (20051229/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details
on the 2005 reload, enter HELP RLOAD at an arrow prompt (=>).
See also:

<http://www.nlm.nih.gov/mesh/>
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate

FILE CAPLUS

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FILE COVERS 1907 - 30 Dec 2005 VOL 144 ISS 2
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***Homo sapiens* Build 35.1**

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Master Map: [Genes On Sequence](#) [Summary of Maps](#)

Maps & Options

Region Displayed: 89,376,720-89,377,580 bp

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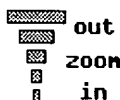
Maps & Options

Compress Map ☐

Region Shown:

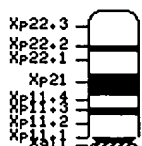
89,376,720

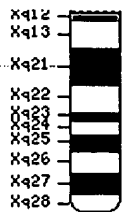
89,377,580



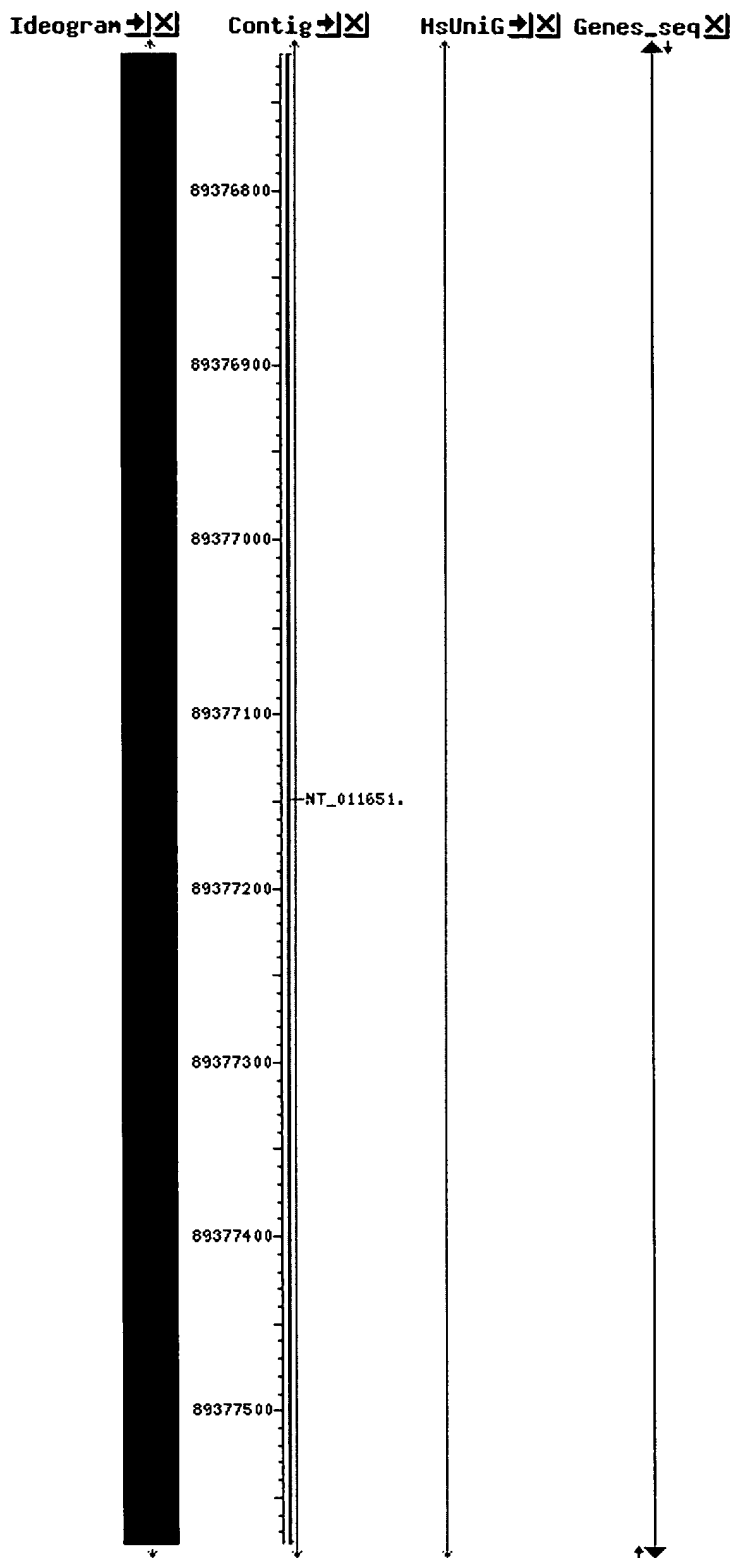
You are here:

Ideogram





- ☒ default
- ☐ master



Summary of Maps:

Map 1: Ideogram

Region Displayed: **Xq21.31**

Map 2: Contig

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total Contigs On Chromosome: **26** [[5 not localized](#)]

Contigs Labeled: **1** Total Contigs in Region: **1**

Map 3: Human UniGene Clusters

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total EST/mRNA alignments On Chromosome: **132438** [[673 not localized](#)]

UniGene Clusters Labeled: **0** Total EST/mRNA alignments in Region: **0**

Histogram Data: Tick Width=**1bp/pixel**, Max Height=**0 transcripts** (logarithmic scale)

Map 4: Genes On Sequence

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total Genes On Chromosome: **1141** [[16 not localized](#)]

Genes Labeled: **0** Total Genes in Region: **0**

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***Homo sapiens* Build 35.1**

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Master Map: Genes On Sequence

Summary of Maps

Maps & Options

Region Displayed: 5,987,242-5,987,747 bp

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Data As Table View

Maps & Options

Compress Map ☐

Region Shown:

5,987,242

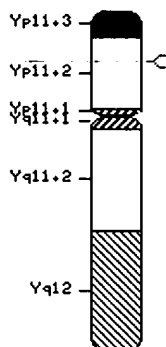
5,987,747

Go

out
zoom
in

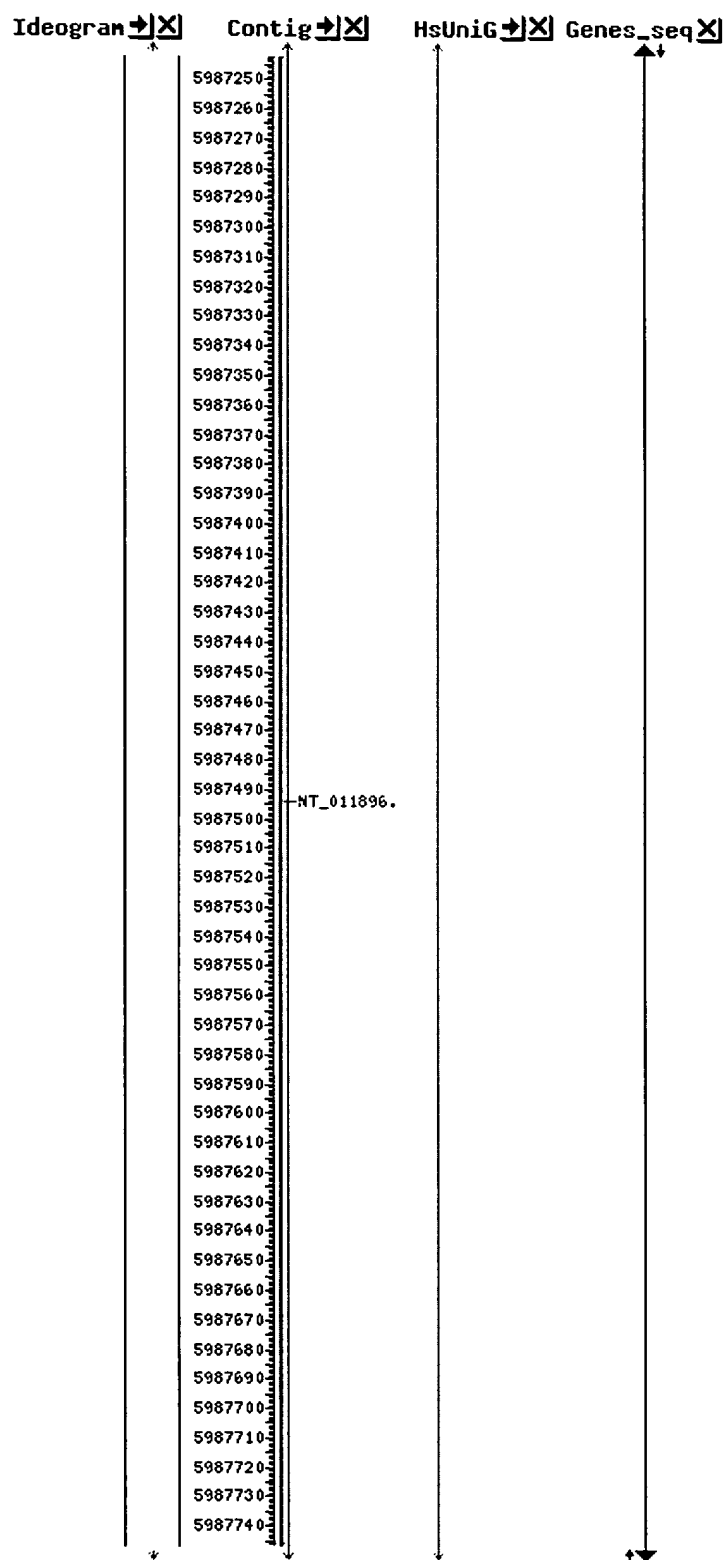
You are here:

Ideogram



☒ default

☐ master



Summary of Maps:

Map 1: Ideogram

Region Displayed: **Yp11.2**

Map 2: Contig

Region Displayed: **5,987,242-5,987,747 bp**

Total Contigs On Chromosome: 17

[Table View](#)

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Contigs Labeled: 1 Total Contigs in Region: 1

Map 3: Human UniGene Clusters

[Table View](#)

Region Displayed: **5,987,242-5,987,747 bp** [Download/View Sequence/Evidence](#)

Total EST/mRNA alignments On Chromosome: **8310**

UniGene Clusters Labeled: **0** Total EST/mRNA alignments in Region: **0**

Histogram Data: Tick Width=**1bp/pixel**, Max Height=**0 transcripts** (logarithmic scale)

Map 4: Genes On Sequence

[Table View](#)

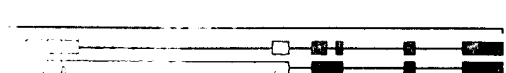
Region Displayed: **5,987,242-5,987,747 bp** [Download/View Sequence/Evidence](#)

Total Genes On Chromosome: **255**

Genes Labeled: **0** Total Genes in Region: **0**

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All: 1 Genes Genomes: 1 SNP GeneView: 1

☐ 1: **ZFX zinc finger protein, X-linked** [*Homo sapiens*]

GeneID: 7543 Primary source: [HGNC:12869](#)

updated 21

Summary

Official Symbol: ZFX and **Name:** zinc finger protein, X-linked provided by HUGO Nomenclature Committee

See related: [HPRD:02445](#), [MIM:314980](#)

Gene type: protein coding

Gene name: ZFX

Gene description: zinc finger protein, X-linked

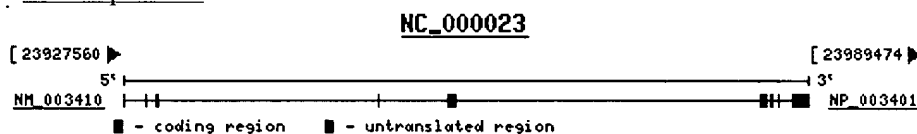
RefSeq status: Validated

Organism: *Homo sapiens*

Lineage: *Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo*

Genomic regions, transcripts, and products

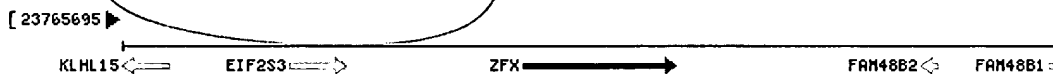
[RefSeq below](#)



Genomic context

[See ZFX in MapViewer](#)

chromosome: X; Location: Xp21.3



Bibliography

Gene References into Function (GeneRIF): [Submit](#)

[PubMed links](#)

General gene information

Markers

G10526(e-PCR) (Links: [UniSTS:38072](#))

Alternate names: CHLC.UTR_01300_X59739; CHLC.UTR_01300_X59739.P3

ZFX(e-PCR) (Links: [UniSTS:99002](#))

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Alternate name: sWXD1468
G42693(e-PCR) (Links: [UniSTS:140880](#))
 Alternate name: sY753
GDB:216882(e-PCR) (Links: [UniSTS:156221](#))
Fabian_Werner_1(e-PCR) (Links: [UniSTS:261928](#))
ZFX_2118(e-PCR) (Links: [UniSTS:281083](#))

GeneOntology

Provided by [GOA](#)

Function	Evidence
DNA binding	IEA
DNA binding	TAS PubMed
metal ion binding	IEA
transcription coactivator activity	TAS PubMed
transcription regulator activity	IEA
zinc ion binding	IEA
Process	
regulation of transcription	IEA
regulation of transcription, DNA-dependent	IEA
Component	
nucleus	IEA

Homology:

Mouse, Rat

[Map Viewer](#)

General protein information

Names: zinc finger protein, X-linked
 zinc finger protein ZFX; X-linked zinc finger protein

NCBI Reference Sequences (RefSeq)

mRNA Sequence [NM_003410](#)

Source Sequence [AC002404](#),[AF454950](#),[M30608](#)

Product [NP_003401](#) zinc finger protein, X-linked

Consensus CDS (CCDS) [CCDS14211.1](#)

Conserved Domains (2) [summary](#)

[COG5048](#): [COG5048](#); [FOG](#): Zn-finger [General function prediction only]

Location: 534 - 667 Blast Score: 98

[pfam04704](#): [Zfx_Zfy_act](#); [Zfx / Zfy transcription activation reg](#)

Location: 78 - 410 Blast Score: 1189

Related Sequences

Nucleotide	Protein
Genomic AF045780	AAL62492
Genomic AF045781	AAC03062
Genomic AF454948	AAL51082
Genomic AF454949	AAL51083
Genomic AY012072	AAG38815

mRNA	AB209892	BAD93129
mRNA	AF454950	AAL51084
mRNA	AF505615	AAM33383
mRNA	AF505616	AAM33384
mRNA	AF505617	AAM33385
mRNA	AF505618	AAM33386
mRNA	AF505619	AAM33387
mRNA	AY072770	AAL67136
mRNA	M30608	AAA61309
mRNA	X59738	CAA42416
mRNA	X59739	CAA42417
mRNA	X59740	CAA42418
	None	P17010
		Q59EB9
		Q8NHZ1
		Q8NHZ2
		Q8NHZ3
		Q8NHZ4
		Q8NHZ5
		Q8WWU0
		Q8WXB7
		Q8WXB8
		Q8WXB9
		Q9BYX9

Additional Links

UniGene [Hs.370424](#)

MIM [314980](#)

HPRD [02445](#)

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SEQ ID 1

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> ☐ gi|51511753|ref|NC_000024.7|NC_000024 ☒ Homo sapiens chromosome (Y) complete sequ
Length=57701691

Score = 46.1 bits (23), Expect = 2e-04
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query	1	CATGTATTTGATGGGGATAGAGG	23
Sbjct	5987242	CATGTATTTGATGGGGATAGAGG	5987264

→
5987242 Alu STX₉

5987747
←

SEQ ID 2

> gi|51511753|ref|NC_000024.7|NC_000024 **D** Homo sapiens chromosome Y, complete sequence
Length=57701691

Score = 46.1 bits (23), Expect = 2e-04
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query	1	CCTTTTCATCCAACCTACCACTGA	23
Sbjct	5987769	CCTTTTCATCCAACCTACCACTGA	5987747

SEQ ID 3

> gi|51511752|ref|NC_000023.8|NC_000023 **D** Homo sapiens chromosome (X), complete sequence
Length=154824264

Score = 50.1 bits (25), Expect = 2e-05
Identities = 25/25 (100%), Gaps = 0/25 (0%)
Strand=Plus/Plus

Query	1	TGAAGAAATTCAGTTCATAGCTTGT	25
Sbjct	89376722	TGAAGAAATTCAGTTCATAGCTTGT	89376746

→
89376722

AluSTXa

89377577
←

SEQ ID 4

> ☒ gi|51511752|ref|NC_000023.8|NC_000023 ☒ Homo sapiens chromosome X, complete sequence
Length=154824264

Score = 46.1 bits (23), Expect = 2e-04
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query	1	CAGGAGATCCTGAGATTATGTGG	23
Sbjct	89377599	CAGGAGATCCTGAGATTATGTGG	89377577